



09/587574

SEQUENCE LISTING

<110> Max-Delbrück-Centrum für Molekulare Medizin

<120> Conductine protein and a related agent for diagnosing
and treating tumor illnesses

<130> 0107-026 US

<140> 09/587,574

<141> 2000-06-05

<150> DE 197 38 205.3

<151> 1997-09-02

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conductine
protein

<400> 1

Met Ser Ser Ala Val Leu Val Thr Leu Leu Pro Asp Pro Ser Ser Ser
1 5 10 15

Phe Arg Glu Asp Ala Pro Arg Pro Pro Val Pro Gly Glu Glu Gly Glu
20 25 30

Thr Pro Pro Cys Gln Pro Ser Val Gly Lys Val Gln Ser Thr Lys Pro
35 40 45

Met Pro Val Ser Ser Asn Ala Arg Arg Asn Glu Asp Gly Leu Gly Glu
50 55 60

Pro Glu Gly Arg Ala Ser Pro Asp Ser Pro Leu Thr Arg Trp Thr Lys
65 70 75 80

Ser Leu His Ser Leu Leu Gly Asp Gln Asp Gly Ala Tyr Leu Phe Arg
85 90 95

Thr Phe Leu Glu Arg Glu Lys Cys Val Asp Thr Leu Asp Phe Trp Phe

100 105 110

Ala Cys Asn Gly Phe Arg Gln Met Asn Leu Lys Asp Thr Lys Thr Leu
115 120 125

Arg Val Ala Lys Ala Ile Tyr Lys Arg Tyr Ile Glu Asn Asn Ser Val
130 135 140

Val Ser Lys Gln Leu Lys Pro Ala Thr Lys Thr Tyr Ile Arg Asp Gly
145 150 155 160

Ile Lys Lys Gln Gln Ile Gly Ser Val Met Phe Asp Gln Ala Gln Thr
165 170 175

Glu Ile Gln Ala Val Met Glu Glu Asn Ala Tyr Gln Val Phe Leu Thr
180 185 190

Ser Asp Ile Tyr Leu Glu Tyr Val Arg Ser Gly Gly Glu Asn Thr Ala
195 200 205

Tyr Met Ser Asn Gly Gly Leu Gly Ser Leu Lys Val Leu Cys Gly Tyr
210 215 220

Leu Pro Thr Leu Asn Glu Glu Glu Trp Thr Cys Ala Asp Leu Lys
225 230 235 240

Cys Lys Leu Ser Pro Thr Val Val Gly Leu Ser Ser Lys Thr Leu Arg
245 250 255

Ala Thr Ala Ser Val Arg Ser Thr Glu Thr Ala Glu Asn Gly Phe Arg
260 265 270

Ser Phe Lys Arg Ser Asp Pro Val Asn Pro Tyr His Val Gly Ser Gly
275 280 285

Tyr Val Phe Ala Pro Ala Thr Ser Ala Asn Asp Ser Glu Leu Ser Ser
290 295 300

Asp Ala Leu Thr Asp Asp Ser Met Ser Met Thr Asp Ser Ser Val Asp
305 310 315 320

Gly Val Pro Pro Tyr Arg Met Gly Ser Lys Lys Gln Leu Gln Arg Glu
325 330 335

Met His Arg Ser Val Lys Ala Asn Gly Gln Val Ser Leu Pro His Phe
340 345 350

Pro Arg Thr His Arg Leu Pro Lys Glu Met Thr Pro Val Glu Pro Ala

355

360

365

Ala Phe Ala Ala Glu Leu Ile Ser Arg Leu Glu Lys Leu Lys Leu Glu
370 375 380

Leu Glu Ser Arg His Ser Leu Glu Glu Arg Leu Gln Gln Ile Arg Glu
385 390 395 400

Asp Glu Glu Lys Glu Gly Ser Glu Gln Ala Leu Ser Ser Arg Asp Gly
405 410 415

Ala Pro Val Gln His Pro Leu Ala Leu Leu Pro Ser Gly Ser Tyr Glu
420 425 430

Glu Asp Pro Gln Thr Ile Leu Asp Asp His Leu Ser Arg Val Leu Lys
435 440 445

Thr Pro Gly Cys Gln Ser Pro Gly Val Gly Arg Tyr Ser Pro Arg Ser
450 455 460

Arg Ser Pro Asp His His His Gln His His His Gln Gln Cys His
465 470 475 480

Thr Leu Leu Ser Thr Gly Gly Lys Leu Pro Pro Val Ala Ala Cys Pro
485 490 495

Leu Leu Gly Gly Lys Ser Phe Leu Thr Lys Gln Thr Thr Lys His Val
500 505 510

His His His Tyr Ile His His Ala Val Pro Lys Thr Lys Glu Glu
515 520 525

Ile Glu Ala Glu Ala Thr Gln Arg Val Arg Cys Leu Cys Pro Gly Gly
530 535 540

Thr Asp Tyr Tyr Cys Tyr Ser Lys Cys Lys Ser His Pro Lys Ala Pro
545 550 555 560

Glu Pro Leu Pro Gly Glu Gln Phe Cys Gly Ser Arg Gly Gly Thr Leu
565 570 575

Pro Lys Arg Asn Ala Lys Gly Thr Glu Pro Gly Leu Ala Leu Ser Ala
580 585 590

Arg Asp Gly Gly Met Ser Ser Ala Ala Gly Gly Pro Gln Leu Pro Gly
595 600 605

Glu Glu Gly Asp Arg Ser Gln Asp Val Trp Gln Trp Met Leu Glu Ser

610 615 620
Glu Arg Gln Ser Lys Ser Lys Pro His Ser Ala Gln Ser Ile Arg Lys
625 630 635 640

Ser Tyr Pro Leu Glu Ser Ala Arg Ala Ala Pro Gly Glu Arg Val Ser
645 650 655

Arg His His Leu Leu Gly Ala Ser Gly His Ser Arg Ser Val Ala Arg
660 665 670

Ala His Pro Phe Thr Gln Asp Pro Ala Met Pro Pro Leu Thr Pro Pro
675 680 685

Asn Thr Leu Ala Gln Leu Glu Glu Ala Cys Arg Arg Leu Ala Glu Val
690 695 700

Ser Lys Pro Gln Lys Gln Arg Cys Cys Val Ala Ser Gln Gln Arg Asp
705 710 715 720

Arg Asn His Ser Ala Ala Gly Gln Ala Gly Ala Ser Pro Phe Ala Asn
725 730 735

Pro Ser Leu Ala Pro Glu Asp His Lys Glu Pro Lys Lys Leu Ala Ser
740 745 750

Val His Ala Leu Gln Ala Ser Glu Leu Val Val Thr Tyr Phe Phe Cys
755 760 765

Gly Glu Glu Ile Pro Tyr Arg Arg Met Leu Lys Ala Gln Ser Leu Thr
770 775 780

Leu Gly His Phe Lys Glu Gln Leu Ser Lys Lys Gly Asn Tyr Arg Tyr
785 790 795 800

Tyr Phe Lys Lys Ala Ser Asp Glu Phe Ala Cys Gly Ala Val Phe Glu
805 810 815

Glu Ile Trp Asp Asp Glu Thr Val Leu Pro Met Tyr Glu Gly Arg Ile
820 825 830

Leu Gly Lys Val Glu Arg Ile Asp
835 840

<210> 2
<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Partial
sequence of conductin protein 78-200 (rgs-domain)

<400> 2

Trp Thr Lys Ser Leu His Ser Leu Leu Gly Asp Gln Asp Gly Ala Tyr
1 5 10 15

Leu Phe Arg Thr Phe Leu Glu Arg Glu Lys Cys Val Asp Thr Leu Asp
20 25 30

Phe Trp Phe Ala Cys Asn Gly Phe Arg Gln Met Asn Leu Lys Asp Thr
35 40 45

Lys Thr Leu Arg Val Ala Lys Ala Ile Tyr Lys Arg Tyr Ile Glu Asn
50 55 60

Asn Ser Val Val Ser Lys Gln Leu Lys Pro Ala Thr Lys Thr Tyr Ile
65 70 75 80

Arg Asp Gly Ile Lys Lys Gln Gln Ile Gly Ser Val Met Phe Asp Gln
85 90 95

Ala Gln Thr Glu Ile Gln Ala Val Met Glu Glu Asn Ala Tyr Gln Val
100 105 110

Phe Leu Thr Ser Asp Ile Tyr Leu Glu Tyr Val
115 120

<210> 3

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Partial
sequence of conductin protein 343-396 (GSK 3B)

<400> 3

Ala Asn Gly Gln Val Ser Leu Pro His Phe Pro Arg Thr His Arg Leu
1 5 10 15

Pro Lys Glu Met Thr Pro Val Glu Pro Ala Ala Phe Ala Ala Glu Leu

20

25

30

Ile Ser Arg Leu Glu Lys Leu Lys Leu Glu Leu Glu Ser Arg His Ser
35 40 45

Leu Glu Glu Arg Leu Gln
50

<210> 4
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial
sequence of conductin protein 397-465 (β -catenine
binding domain)

<400> 4
Gln Ile Arg Glu Asp Glu Glu Lys Glu Gly Ser Glu Gln Ala Leu Ser
1 5 10 15

Ser Arg Asp Gly Ala Pro Val Gln His Pro Leu Ala Leu Leu Pro Ser
20 25 30

Gly Ser Tyr Glu Glu Asp Pro Gln Thr Ile Leu Asp Asp His Leu Ser
35 40 45

Arg Val Leu Lys Thr Pro Gly Cys Gln Ser Pro Gly Val Gly Arg Tyr
50 55 60

Ser Pro Arg Ser Arg
65

<210> 5
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Partial
sequence of conductin protein 783-833 (dishevelled
homologue region)

<400> 5

Leu Thr Leu Gly His Phe Lys Glu Gln Leu Ser Lys Lys Gly Asn Tyr
1 5 10 15

Arg Tyr Tyr Phe Lys Lys Ala Ser Asp Glu Phe Ala Cys Gly Ala Val
20 25 30

Phe Glu Glu Ile Trp Asp Asp Glu Thr Val Leu Pro Met Tyr Glu Gly
35 40 45

Arg Ile Leu
50

<210> 6

<211> 2825

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA of
conductine protein

<400> 6

cagccgttcg cgatggattt cggggccacc cggaggccga ggcgtccggc tccccaaagg 60
agagctttgc tgtaaaaagag aggaggctca catgagcccc tgctgactta agagagacca 120
agccgattgc tgagaggaac tggagaaga aaaaggagga ggagggaaaa aaagcaaaaac 180
aaaatccaaa ctcagtgaga cgctctccct caccatgagt agcgcgtgt tagtgactct 240
ccttccagat cccagcagca gcttccgcga ggatgctccg cggcccccgg ttccgggaga 300
agaagggag accccaccgt gtcagcctag tggggcaag gtccagtcca ccaaacctat 360
gcccgttcc tctaattgta ggcggaatga agatggactg ggggagcccgg aggggcgggc 420
ctcccccgat tccccttga ccaggtggac caagtcttta cactccttgt tgggtgacca 480
ggatggtgca tacctcttcc ggactttctt ggagagggag aaatgtgtgg atacgctgga 540
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agtggccaaa gcaatctata agaggtacat tgagaacaac agcgttgtct ccaagcagct 660
gaagccgccc accaagacct acatacgaga tggcatcaag aagcaacaga tcggctcggt 720
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aggcaggatc ctggccaaag tggagaggat cgactgagcc ttggccctcct cggcgtgcaa 2760
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tacgc 2825

<210> 7
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cDNA partial
sequence 446-814

<400> 7
tggaccaagt cttaacactc cttgttgggt gaccaggatg gtgcataacct cttccggact 60
ttcctggaga gggagaaatg tgtggatacg ctggacttct ggtttgcctt taatgggttc 120
aggcagatga acctgaagga tacaaaaact ttgcgagtgg ccaaagcaat ctataagagg 180
tacattgaga acaacagcgt tgtctccaag cagctgaagc cggccaccaa gacctacata 240
cgagatggca tcaagaagca acagatggc tcggcatgt ttgaccaggc acagaccgag 300
atccaggcag tcatggagga aaatgcctac caggtgttct tgacttctga catttacctg 360
gaatatgtg 369

<210> 8
<211> 162

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA partial
sequence 1241-1402

<400> 8

gc caatggcc aagtgtctct acctcatttt ccgagaaccc accgcctgcc caaggagatg 60
acgcctgtgg aacctgctgc ctgcgccccc gagctcatct ccaggctgga gaaactgaaa 120
ctggagctgg aaagccqcca tagtctggag gagcggctgc ag 162

<210> 9

<211> 207

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA partial
sequence 1403-1609

<400> 9

cagatccggg aggatgaaga aaaggagggg tctgagcagg ccctgagctc acgggatgga 60
gcaccgggtcc agcacccccct ggccctccta ccctccggca gctatgaaga ggacccacaa 120
accatttgg acgaccaccc ctccagggtc ctcaagaccc ccggctgtca atcccctgg 180
gtgggtcgct acagccccacg gtccccgc 207

<210> 10

<211> 153

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA partial
sequence 2561-2713

<400> 10

ttgaccctgg gccacttcaa ggagcagctc agcaaaaagg gaaattacag gtattatttc 60
aagaaggcga gtgacgaatt tgccctgcggc gcagtttttg aggagatctg ggacgacgag 120
acagtgtcc ccatgtacga aggcaggatc ctg 153